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In the Claims

Kindly amend Claims 63 and 104 and add new Claims 110-113 as follows:

STATUS OF THE CLAIMS

1-31. (Canceled)

32. (Previously presented) The method of claim 63, 84, 85, 88, or 106 wherein at least 50% by weight of all proteins in the sample are removed.

33-51. (Canceled)

52. (Previously presented) The method of claim 63, 84, or 85, further comprising the step of analyzing a plurality of proteins remaining in the modified sample.

53-61. (Canceled)

62. (Previously presented) The method of claim 63, 84, or 85, wherein at least one of the specific predefined proteins is present at higher abundance than at least one of the plurality of proteins remaining in the sample after removal of the specific predefined proteins.

63. (Currently amended) A method for separating proteins from a sample that contains proteins and recovering a modified sample for analysis of remaining proteins comprising:

removing at least two specific predefined proteins from a sample that contains the at least two specific predefined proteins, thereby producing a modified sample containing a plurality of proteins that was present in the sample prior to removal of the at least two specific predefined proteins; and

recovering the modified sample,

wherein the removing step comprises contacting the sample with an affinity binding composition comprising:

a first and a second solid phase matrix contacting each other, wherein each solid phase matrix comprises a plurality of particles, and wherein the particles of the first and second solid phase matrices are present as a mixture in said affinity binding composition;

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a first receptor immobilized on said first solid phase matrix, capable of specific binding to a first protein but not a second protein; and

a second receptor immobilized on said second solid phase matrix, capable of specific binding to the second protein but not the first protein.

64. (Previously presented) The method of claim 63, wherein the affinity binding composition further comprises:

a third receptor immobilized on a third solid phase matrix, capable of specific binding to a third protein but not the first protein or the second protein.

65. (Previously presented) The method of claim 64, wherein the third solid phase matrix contacts the first and second solid phase matrices.

66. (Previously presented) The method of claim 63, wherein the affinity binding composition further comprises: a fourth receptor immobilized on a fourth solid phase matrix, capable of specific binding to a fourth protein but not the first protein, the second protein or the third protein.

67. (Previously presented) The method of claim 66, wherein the fourth solid phase matrix contacts the first, second, and third solid phase matrices.

68. (Previously presented) The method of claim 67, wherein the affinity binding composition further comprises:

a fifth receptor immobilized on a fifth solid phase matrix, capable of specific binding to a protein but not the first protein, the second protein, the third protein or the fourth protein.

69. (Previously presented) The method of claim 68, wherein the fifth solid phase matrix contacts the first, second, third, and fourth solid phase matrices.

70-83. (Canceled)

84. (Previously presented) A method for separating proteins from a sample that contains proteins and recovering a modified sample for analysis of remaining proteins comprising:

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removing at least two specific predefined proteins from a sample that contains the at least two specific predefined proteins, thereby producing a modified sample containing a plurality of proteins that was present in the sample prior to removal of the at least two specific predefined proteins; and

recovering the modified sample,

wherein the removing step comprises contacting the sample with an affinity binding composition comprising:

a plurality of solid phase matrices arranged such that each solid phase matrix is in contact with at least one other solid phase matrix; and

a plurality of receptors having different protein binding specificities, wherein the receptors are immobilized on the plurality of solid phase matrices such that each solid phase matrix has a different protein binding specificity, wherein each solid phase matrix comprises a plurality of particles, and wherein the particles are present in the affinity binding composition as a mixture.

85. (Previously presented) The method of claim 63, or 84, wherein the sample is passed through a column containing the affinity binding composition to produce the modified sample, wherein the affinity column has a fluid inlet and a fluid outlet, and wherein the modified sample is collected at the fluid outlet.

86-87. (Canceled)

88. (Previously presented) The method of claim 63, 84, or 85, wherein the receptors are antibodies or antibody fragments that specifically bind to the specific, predefined proteins.

89. (Previously presented) The method of claim 63, 84, or 85, wherein the receptors are recombinantly produced.

90-103. (Canceled)

104. (Currently amended) The method of claim 63, 84, or 85, wherein at least one of the specific predefined proteins is selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein,

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myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin, and combinations thereof.

105. (Previously presented) The method of claim 63, 84, or 85, wherein at least two of the specific predefined proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin.

106. (Previously presented) The method of claim 63, 84, 85, or 88, wherein at least three of the specific predefined proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin.

107. (Previously presented) The method of claim 63, 84, or 85, wherein at least four of the specific predefined proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein A1, α_2-macroglobulin, fibrinogen, and prealbumin.

108 – 109. (Canceled)

110. (NEW) The method of claim 63, wherein at least three specific predefined proteins are removed from a sample.

111. (NEW) The method of claim 84, wherein at least three specific predefined proteins are removed from a sample.

112. (NEW) The method of claim 63, wherein at least four specific predefined proteins are removed from a sample.

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113. (NEW) The method of claim 84, wherein at least four specific predefined proteins are removed from a sample.

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